



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:45 AM UTC

PDB ID : 8AMR / pdb_00008amr
Title : Coiled-coil domain of human TRIM3
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Deposited on : 2022-08-04
Resolution : 3.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

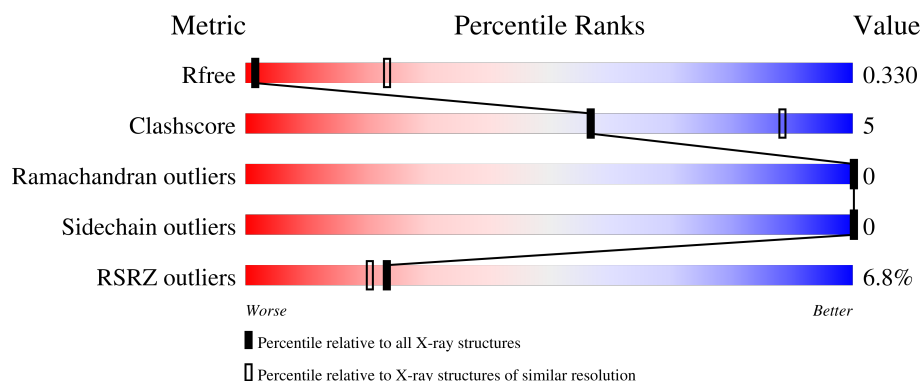
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	319	
1	B	319	
1	C	319	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6137 atoms, of which 2872 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

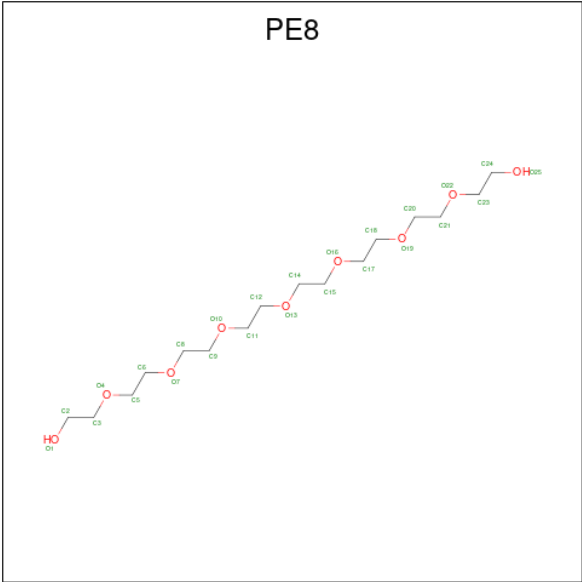
- Molecule 1 is a protein called Tripartite motif-containing protein 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	155	Total	C	H	N	O	S	0	0	0
			2131	692	1003	209	224	3			
1	B	154	Total	C	H	N	O	S	0	0	0
			2013	667	942	191	211	2			
1	C	147	Total	C	H	N	O	S	0	0	0
			1965	643	927	190	202	3			

There are 9 discrepancies between the modelled and reference sequences:

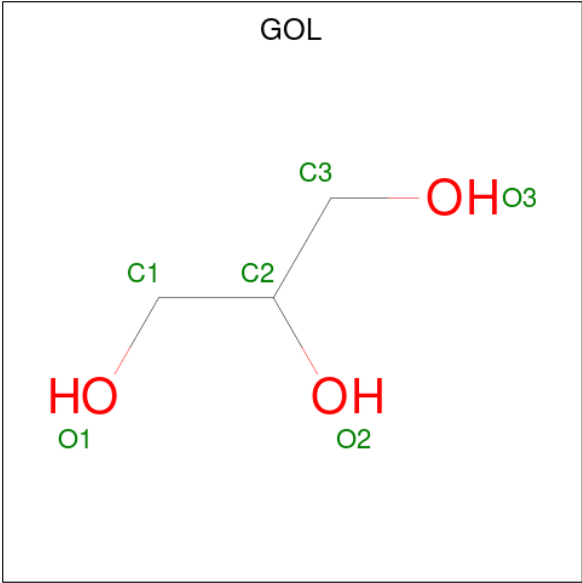
Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLY	-	expression tag	UNP O75382
A	5	ALA	-	expression tag	UNP O75382
A	6	MET	-	expression tag	UNP O75382
B	4	GLY	-	expression tag	UNP O75382
B	5	ALA	-	expression tag	UNP O75382
B	6	MET	-	expression tag	UNP O75382
C	4	GLY	-	expression tag	UNP O75382
C	5	ALA	-	expression tag	UNP O75382
C	6	MET	-	expression tag	UNP O75382

- Molecule 2 is 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL (CCD ID: PE8) (formula: C₁₆H₃₄O₉).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).

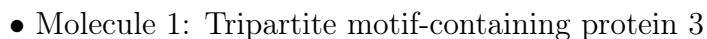


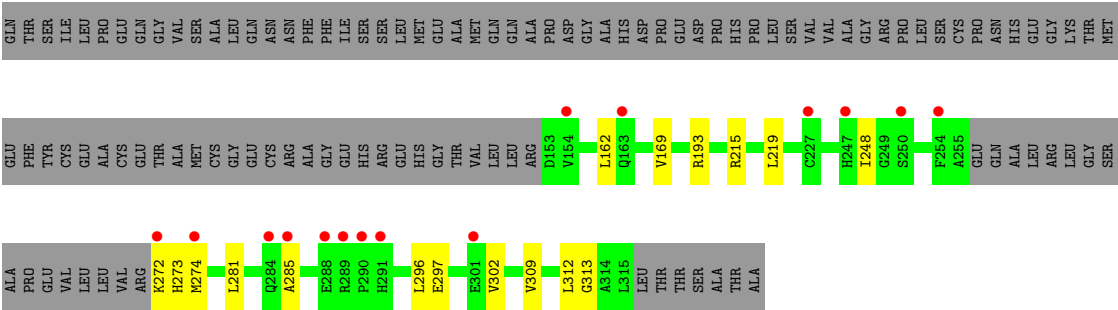
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	O 2	0	0
4	B	4	Total 4	O 4	0	0
4	C	3	Total 3	O 3	0	0

- Molecule 1: Tripartite motif-containing protein 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	167.90Å 167.90Å 127.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.53 – 3.80 48.53 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.53-3.80) 93.7 (48.53-3.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.43 (at 3.67Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.273 , 0.321 0.273 , 0.330	Depositor DCC
R_{free} test set	989 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	169.1	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 183.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6137	wwPDB-VP
Average B, all atoms (Å ²)	192.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PE8, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.08	0/1134	0.25	0/1532
1	B	0.07	0/1079	0.22	0/1468
1	C	0.07	0/1044	0.22	0/1415
All	All	0.07	0/3257	0.23	0/4415

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1128	1003	1089	3	0
1	B	1071	942	1003	19	0
1	C	1038	927	997	21	0
2	B	13	0	17	1	0
3	B	6	0	8	0	0
4	A	2	0	0	0	0
4	B	4	0	0	2	0
4	C	3	0	0	0	0
All	All	3265	2872	3114	29	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 5.

All (29) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:501:HOH:O	1:C:297:GLU:HB2	1.63	0.95
1:B:313:GLY:HA3	1:C:219:LEU:HD11	1.74	0.70
1:A:275:ARG:NH2	1:C:274:MET:SD	2.66	0.67
1:B:196:GLU:OE2	1:C:296:LEU:HD21	1.96	0.66
1:B:306:ARG:O	1:B:309:VAL:HG12	2.00	0.61
1:B:219:LEU:HD11	1:C:313:GLY:HA3	1.84	0.59
1:B:208:LEU:HD11	1:C:302:VAL:HG13	1.86	0.57
1:B:313:GLY:O	1:C:215:ARG:NH2	2.39	0.56
1:B:193:ARG:HB3	1:C:296:LEU:HD23	1.89	0.54
1:B:201:ILE:CD1	1:C:219:LEU:HD13	2.38	0.54
1:B:315:LEU:HA	1:C:297:GLU:O	2.08	0.53
1:A:167:GLU:HA	1:A:170:ARG:HE	1.76	0.49
1:B:215:ARG:NH2	1:C:312:LEU:O	2.44	0.49
1:B:234:LEU:HD21	1:B:292:GLU:HB3	1.95	0.48
1:B:278:LEU:HD22	1:C:169:VAL:HG11	1.95	0.48
1:A:243:GLN:NE2	1:C:285:ALA:O	2.45	0.47
1:C:193:ARG:O	1:C:193:ARG:HD2	2.16	0.46
1:B:312:LEU:HD23	1:B:313:GLY:N	2.32	0.45
1:B:195:ALA:HA	1:B:198:LEU:HD12	1.98	0.45
1:B:264:ALA:HB3	1:B:265:PRO:HD3	2.00	0.44
1:B:305:LEU:HD21	1:C:309:VAL:HG22	2.00	0.43
1:C:272:LYS:O	1:C:273:HIS:CB	2.66	0.43
2:B:401:PE8:H202	2:B:401:PE8:H231	1.72	0.43
1:B:248:ILE:HG13	1:B:281:LEU:HD22	2.01	0.42
1:C:248:ILE:HG13	1:C:281:LEU:HD22	2.02	0.41
1:B:193:ARG:HD3	1:C:296:LEU:HD23	2.02	0.41
1:B:278:LEU:HD12	1:C:162:LEU:HD11	2.02	0.41
4:B:501:HOH:O	1:C:297:GLU:CB	2.43	0.40
1:C:296:LEU:HD12	1:C:296:LEU:C	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	151/319 (47%)	146 (97%)	5 (3%)	0	100	100
1	B	150/319 (47%)	144 (96%)	6 (4%)	0	100	100
1	C	143/319 (45%)	135 (94%)	8 (6%)	0	100	100
All	All	444/957 (46%)	425 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	107/265 (40%)	107 (100%)	0	100	100
1	B	95/265 (36%)	95 (100%)	0	100	100
1	C	96/265 (36%)	96 (100%)	0	100	100
All	All	298/795 (38%)	298 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS
1	A	213	GLN
1	B	245	GLN
1	C	245	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PE8	B	401	-	12,12,24	0.55	0	11,11,23	0.51	0
3	GOL	B	402	-	5,5,5	0.33	0	5,5,5	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PE8	B	401	-	-	5/10/10/22	-
3	GOL	B	402	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	402	GOL	O1-C1-C2-C3
2	B	401	PE8	O16-C17-C18-O19

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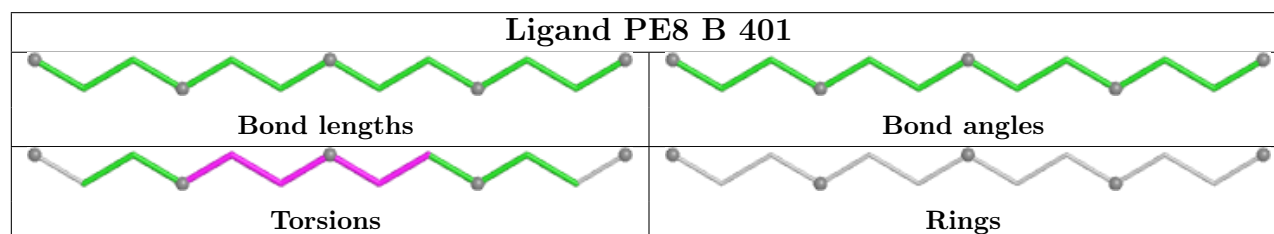
Mol	Chain	Res	Type	Atoms
2	B	401	PE8	O19-C20-C21-O22
3	B	402	GOL	O1-C1-C2-O2
2	B	401	PE8	C20-C21-O22-C23
2	B	401	PE8	C17-C18-O19-C20
2	B	401	PE8	C21-C20-O19-C18

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	PE8	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	155/319 (48%)	0.45	11 (7%) 22 19	132, 191, 240, 284	0
1	B	154/319 (48%)	0.37	5 (3%) 50 35	135, 193, 235, 286	0
1	C	147/319 (46%)	0.62	15 (10%) 12 14	144, 190, 231, 248	0
All	All	456/957 (47%)	0.48	31 (6%) 23 20	132, 192, 236, 286	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	288	GLU	5.2
1	C	290	PRO	5.1
1	A	258	ALA	4.7
1	C	154	VAL	3.9
1	A	318	THR	3.6
1	C	301	GLU	3.5
1	C	254	PHE	3.4
1	C	274	MET	3.3
1	A	247	HIS	3.2
1	B	267	VAL	3.1
1	B	225	THR	3.0
1	C	227	CYS	2.8
1	A	295	GLN	2.8
1	C	289	ARG	2.7
1	B	273	HIS	2.7
1	A	291	HIS	2.6
1	A	222	ASP	2.5
1	C	250	SER	2.5
1	B	190	LEU	2.4
1	A	275	ARG	2.4
1	C	285	ALA	2.4
1	A	277	ARG	2.4
1	A	254	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	291	HIS	2.3
1	A	272	LYS	2.3
1	C	272	LYS	2.3
1	C	247	HIS	2.2
1	C	163	GLN	2.2
1	B	160	ALA	2.1
1	A	294	ALA	2.0
1	C	284	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

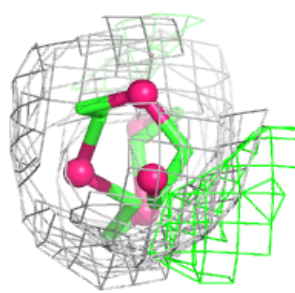
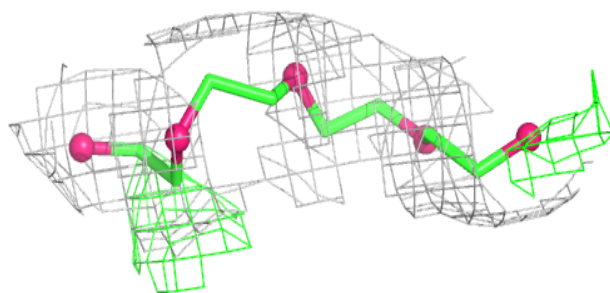
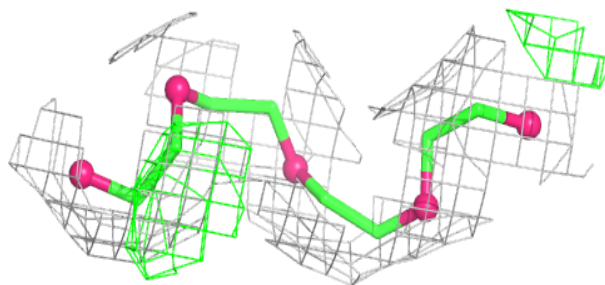
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	402	6/6	0.53	0.14	179,217,231,248	0
2	PE8	B	401	13/25	0.81	0.24	130,165,209,223	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PE8 B 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.